

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Wei-Wu He, Kristine K. Kikly, Vishva M. Dixit, Steven M. Ruben

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOSIS PROTEASE-6

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: SmithKline Beecham Corporation
- (B) STREET: 709 Swedeland Road
- (C) CITY: King of Prussia
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: UNKNOWN
- (B) FILING DATE: HEREWITH
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/018,961
- (B) FILING DATE: 05 JUNE 1996

- (A) APPLICATION NUMBER: 60/020,344
- (B) FILING DATE: 23 MAY 1996

- (A) APPLICATION NUMBER: 60/017,949
- (B) FILING DATE: 20 May 1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Han, William T.
 (B) REGISTRATION NUMBER: 34,344
 (C) REFERENCE/DOCKET NUMBER: P50483-2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5219
 (B) TELEFAX: 610-270-5090
 (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Glu	Ala	Asp	Arg	Arg	Leu	Leu	Arg	Arg	Cys	Arg	Leu	Arg	Leu
1					5				10					15	
Val	Glu	Glu	Leu	Gln	Val	Asp	Gln	Leu	Trp	Asp	Val	Leu	Ser	Arg	
					20				25				30		
Glu	Leu	Phe	Arg	Pro	His	Met	Ile	Glu	Asp	Ile	Gln	Arg	Ala	Gly	Ser
					35				40			45			
Gly	Ser	Arg	Arg	Asp	Gln	Ala	Arg	Gln	Leu	Ile	Ile	Asp	Leu	Glu	Thr
					50				55			60			
Arg	Gly	Ser	Gln	Ala	Leu	Pro	Leu	Phe	Ile	Ser	Cys	Leu	Glu	Asp	Thr
					65				70			75		80	
Gly	Gln	Asp	Met	Leu	Ala	Ser	Phe	Leu	Arg	Thr	Asn	Arg	Gln	Ala	Gly
					85				90			95			
Lys	Leu	Ser	Lys	Pro	Thr	Leu	Glu	Asn	Leu	Thr	Pro	Val	Val	Leu	Arg
					100				105			110			
Pro	Glu	Ile	Arg	Lys	Pro	Glu	Val	Leu	Arg	Pro	Glu	Thr	Pro	Arg	Pro
					115				120			125			
Val	Asp	Ile	Gly	Ser	Gly	Gly	Phe	Gly	Asp	Val	Gly	Ala	Leu	Glu	Ser
					130				135			140			

Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 285
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365
 Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGACG	AAGCGGATCG	GCGGCTCTG	CGGCCTGCC	GGCTGCCGCT	GGTGGAAAGAG	60
CTGCAGTGG	ACTAGCTCTG	GGACGTCTG	CTGAGCGGCC	AGCTGTCAG	GCCCCATATA	120
ATCGAGACA	TCCAGCGGC	AGGCTCTGGA	TCTCGGGGG	ATCAGGCCAG	GCAGCTGATC	180
ATAGATCTGG	AGACTCGAGG	CAGTCAGGCT	CTTCCTTTGT	TCATCTCTG	CITAGAGGAC	240
ACAGGCCAGG	ACATGCTGGC	TTCTGTTCTG	CGAACTAACAA	GGCAAGCAGG	AAAGTTGTCG	300
AAGCCAACCC	TAGAAAACCT	TACCCCAGTG	GTGCTCAGAC	CAGAGATTG	CAAACCAGAG	360
GTTCCTCAGAC	CGGAAACACC	CAGACAGCTG	GACATTGGTT	CTGGAGGATT	CGGTGATGTC	420
GGTGGCTTGTG	AGAGTCTGAG	GGGAAATGCA	GAATTGGCTT	ACATCTGAG	CATGGAGCCC	480
TGTGGCCACT	CTTCATGAT	CAACATCTG	AACTCTGTC	GTGAGTCGCC	GCTCCGCACC	540
CGCACTGGCT	CCAACATCGA	CTGTGAGGAG	TTGGCGCTG	GCTTCTCTC	GCTGCATTC	600
ATGGTGGAGG	TGAGGGCGA	CCTGACTGC	AAAGAAAATGG	TGCTGGCTTT	GCTGGAGCTG	660
GCGCGGCAGG	ACCACGGTGC	TCTGGACTGC	TGCGTGGTGG	TCATTCTCTC	TCACGGCTGT	720
CAGGCCAGCC	ACCTGAGCTT	CCACGGGCT	GTCCTAGGCC	CAGATGGATG	CCCTGTGTCG	780
GTCAGGAAGA	TTGTGAAACAT	CTTCATGGG	ACCACTGCGC	CCAGCTGGG	AGGGAAAGCCC	840
AAGCTCTTTT	TCATCCGGC	CTGTTGGGG	GAGCAGAAAG	ACCATGGTTT	TGAGGTGGCC	900
TCCACTTCCC	CTGAAGACGA	GTTCCTCTGG	AGTAACCCC	AGCCAGATGC	CACCCCGTTC	960
CAGGAAGGTT	TGAGGACCTT	CGACCAAGTG	GACGCCATAT	CTAGTTGCC	CACACCCAGT	1020
GACATTTTG	TGTCTACTC	TACTTTCCA	GGTTTTGTTT	CCTGGAGGGA	CCCCAAGAGT	1080
GGCTCTCTGT	ACCTTGAGAC	CTTGGACGAC	ATCTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
CTGCGATCCC	TCTCTGTTAG	GTCGCTTAAT	GCTGTTTCGG	TGAAAGGGAT	TTATAAACAG	1200
ATGCCCTGGT	GCTTTAATT	CCTCCGGGG	AAACTTTCT	TTAAAACATC	ATAAGGCCAG	1260
GGCCCCCTAC	CTTGCCTTAT	CTTGACCCCC	AAAGCTTCTC	TGCCCCAGGC	CTGAAAGAGG	1320
CTGAGGCCCTG	GAATTCTCTG	CAACTCAAGC	ACTTTGNAGC	CGGCACAGGG	TCTGCTCTT	1380
CTCTGCCAGT	GACAGACAGG	CTCTTAGCAG	CTTCCAGATT	GACGACAAGT	GCTGAACAGT	1440
GGAGGAAGAG	GGACAGATGA	ATGCCGTGGA	TTGCACGTTG	NCTCTTGAGC	AGTGGCTGTT	1500
CCAGGGCTAG	TGACTTGGT	TCCCATGATC	CCTGTGTTGG	TCTCTAGGAG	CAGGGTAA	1560
CCTCTGCACT	ACTGACAT					1578

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA AGAAAATGGT GCTGGGTTTG CTGGAGCTGG CGCGGCAGGA CCACGGTGT	60
CTGGACTGCT GCGTGGTGGT CATTCTCTCT CACGGCTGTC AGGCCAGCCA CCTGCAGTTC	120
CCAGGGCTG TCTACGGCAC AGATGGATGC CCTGTGTCGG TCGAAAAGAT TGTGAACATC	180
TTCAATGGGA CCAGCTGCC CAGGCTGGG GGGAAAGCCCA AGCTCTTTT CATCCAGGCC	240
TGTGTTGGG AGCAGAAAAGA CCATGGGTTT GAGGTGGCTT CCACCTCCCC TGAAAGACGAG	300
TCCCCGGCA GTAACCCCGA GCCAGATGCC ACCCCGTTCC AGGAAGGTTT GAGGACCTTC	360
GACCAGCTGG ACGCCATATC TAGTTTCCC ACACCCAGTG ACATCTTGT GTCTTACTCT	420
ACTTTCCAG GTTTTGTTC CTGGAGGGAC CCCAAGAGTG GCTCTGGTA CGTTGAGACC	480
CTGGACGACA TCTTTGAGCA GTGGGCTCAC TCTGAAGACC TGCAGTCCCT CCTGCTTAGG	540
GTCGCTAATG CTGTTTGGT GAAAGGGATT TATAAACAGA TGCCTGGTTG CTTTAATTTC	600
CTCCGGAAAA AACTTTCTT TTAAAACATC ATAAGGCG	639

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu
   1           5           10          15
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His
   20          25          .       30
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser
   35          40          .       45
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu
   50          55          .       60
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln

```

65	70	75	80
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser			
85	90	95	
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu			
100	105	110	
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser			
115	120	125	
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg			
130	135	140	
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe			
145	150	155	160
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val			
165	170	175	
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys			
180	185	190	
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met			
195	200		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CGGCCATGGA CGAACCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATGTTTTA AAGAAAAGTT TTTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT TCATCCAGGC CGCGGGTGGG GAGCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCCG CGGCCTGGAT GAAAAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCA CGTCGTCCTT GTAGTCTGAT GTTTTAAAGT TAAGTTTTT
CCGGAG

60

66

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: DIXIT, VISHVA M.
HE, WEI-WU
KCKLY, KRISTINE K.
RUBEN, STEVEN M.

(ii) TITLE OF THE INVENTION: INTERLEUKIN-1 BETA CONVERTING
ENZYME LIKE APOPTOTIC PROTEASE-6

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Rather & Prestia
(B) STREET: P.O. Box 980
(C) CITY: Valley Forge
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19482

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/952,936
(B) FILING DATE: 08-MAY-1997
(C) CLASSIFICATION: UNKNOWN

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/019,361
(B) FILING DATE: 05-JUN-1996

(A) APPLICATION NUMBER: 60/020,344
(B) FILING DATE: 23-MAY-1996

(A) APPLICATION NUMBER: 60/017,949
(B) FILING DATE: 20-MAY-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Prestia, Paul F
(B) REGISTRATION NUMBER: 23,031
(C) REFERENCE/DOCKET NUMBER: p50483-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-407-0700
(B) TELEFAX: 610-407-0700
(C) TELEX: 346169

(x) INFORMATION FOR SEQ ID NO:1: -

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(a) MOLECULE TYPE: protein

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Glu Ala Asp Arg Arg Leu Leu Arg Arg Cys Arg Leu Arg Leu
 1 5 10 15
 Val Glu Glu Leu Gln Val Asp Gln Leu Trp Asp Val Leu Leu Ser Arg
 20 25 30
 Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
 35 40 45
 Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Asp Leu Glu Thr
 50 55 60
 Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
 65 70 75 80
 Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Gly
 85 90 95
 Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
 100 105 110
 Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
 115 120 125
 Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
 130 135 140
 Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
 145 150 155 160
 Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
 165 170 175
 Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
 180 185 190
 Arg Phe Ser Ser Leu His Phe Met Val Gln Val Lys Gly Asp Leu Thr
 195 200 205
 Ala Lys Lys Met Val Leu Ala Leu Leu Gln Leu Ala Arg Gln Asp His
 210 215 220
 Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
 225 230 235 240
 Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
 245 250 255
 Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
 260 265 270
 Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
 275 280 295
 Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
 290 295 300
 Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
 305 310 315 320
 Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
 325 330 335
 Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
 340 345 350
 Ser Trp Arg Asp Pro Lys Ser Gln Ser Trp Tyr Val Glu Thr Leu Asp
 355 360 365

Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
 370 375 380
 Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
 385 390 395 400
 Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
 405 410 415

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCATGGGACG	RAGCGGGATCG	GCCTGGCTCTG	GGCGCGGTGCC	GGCTGCGGGCT	GTTGGAAGAG	60
CTGAGGTGG	ACCAGCTGTG	GGACGCTCTG	CTGAGCGCGG	AGCTGTTTCAG	GCCCCATATG	120
ATCGAGGACA	TGCAAGGGGG	AGGCTCTTGA	TCTGGGGGGG	ATCAGGCCAG	GCAGCTGATC	180
ATAGATCTGG	AGACTCGGAG	GAGTCAGGCT	CTTCCTTTGT	TCATCTCTG	CTTAGAGGAC	240
ACAGCGGAGG	ACATGCTGGC	TGCTGGGGCT	CGAACTAACG	GGCAGCGGAG	AAAGTTGTCG	300
AAGCCACCC	TAGAAAACCT	TACCCCATG	GTGCTCTGAC	CAGAGACTCG	CAACCCAGAG	360
GTTCCTCGAC	CGGAAACACG	CAGACCGATG	GACATTGGTT	CTGGGAGGATT	CGGTGATGTC	420
GGTGTCTTCA	AGAGTTTGAG	GGGAAATGCA	GATTGGGTT	ACATCTCTGAG	CATGGAGGCC	480
TGTGGCCACT	GGCTCAATTAT	CAACATGATG	AACTCTGCGC	GTGAGTCGGG	GTCTGGCACCG	540
CGCACTGGCT	CCAACTATGGA	CTGTGAGAAG	TCTGGCGCTG	GTCTCTCTC	GCTTCATTTG	600
ATGGTGGAGG	TGAAGGGGGC	CTCTACTGCC	AAAGAAATGG	TGCTGGGTTT	GCTGGAGCTG	660
GCCTGGGAGG	ACCCAGGTCG	TCTGGACTGC	TGGTGGTGTG	TCATTCCTCTC	TCACGGCTGT	720
CAGGGCAGCC	ACCTGGCACTT	CCACAGGGCT	CTCTACGGCA	CAGATGGGATG	CCCTGTGTCG	780
GTCAAGAAGA	TGTGAACAT	CTTCATGGG	ACCACTGCGC	CCACGCTGGG	AGGGAAAGCCC	840
AAAGCTTTTT	TGATCAGGGC	CTGGGGTGGG	GGCGAGAAAG	ACCATGGGGTT	TGAGGTGGCC	900
TGGACTCTCC	CTGARGAGGC	TGCCCCCTGGG	TAACCTCCCG	AGCCAGATGC	CACCCGGTTG	960
CAGGAAGGT	TGAGGACCTT	CGGACAGCTT	GACGCGATAT	CTAGTTTGC	CAACCCAGT	1020
GACATCTTTG	TGCTCTACTCT	FACTTTTCCA	TTTTTTTTTT	CTCTGGAGGGA	CCCCAAAGAGT	1080
GGCCTCTGGT	AGCTTGAGAC	CCTGGAGCGA	ACCTTTGAGC	AGTGGGCTCA	CTCTGAAGAC	1140
CTGGAGTCCTC	TCTCTGCTTAG	GGTGCCTAAT	GGTGTGTCG	TGAAAGGGAT	TTATAAACAG	1200
ATGGCTGGT	GCTTTAATT	CTCTCGCTAA	AAACCTTTCT	TTAAACATC	ATAAGGCCAG	1260
GGCCCTCTCAC	CTGGCTCTAT	CTTGACCCCC	AAAGCTTTCC	TGCCCTCAGGC	CTGAAAGAGG	1320
CTGAGGGCTG	GACTCTCTCTG	CAACTCAAGG	ACCTTGTGAGC	GGGCACAGGG	TCTGGCTCTTT	1380
CTCTGCCAGT	GGACAGACAGG	CTCTTACGGC	CTTCCAGATT	GACCGACAACT	GCTGAAACAGT	1440
GGAGGAAGAG	GGACAGATGA	ATGCCGTGGA	TTGCACGTGG	NCTCTTGAGC	AGTGGCTGGT	1500
CCAGGGCTAG	TGACTTGGTG	TCCCATGATC	CTCTGTTGG	TCTCTAGGAG	CAGGGATTA	1560
CCTCTGCACT	ACTGACAT					1578

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGACTGCCA	AGAAAATGGT	GCTGGCTTTG	CTGGAGGTGG	CGCCGCAGGA	CCACCGGTGCT	60
CTGGACTGCT	CGCTGGTGGT	CATTCTCTCT	CACGGCTGTC	AGGCCAGCCA	CTGCAAGTTTC	120
CCAGGGCTG	TCTACGGCAG	AGATGGATGC	CCTTGTGGCA	TGAAAGAT	TGTGAACATC	180
TTCAATGGGA	CCAGCTGGCA	CCAGCTGGGA	GGGAGGCCC	AGCTCTTTT	CATCCAGGCC	240
TGTTGGGGGG	AGCAGAAAAGA	CCATGGGTTT	GAGGTGGCCC	CCACTCCSC	TGAAGACGAG	300
TCCCCCTGGCA	GTAAACCCCGA	GGCAGATGCC	ACCCCGTTCC	AGGAAGGTTT	GAGGACCTTC	360
GACCAAGCTGG	ACGCCATATC	TAGTTGGCC	ACACCGAGTG	ACATCTTGT	GTCTCTACTCT	420
ACTTTCCAG	GTTTGTTTC	CTGGAGGGAC	CCCAAGAGTG	GCTCCCTGGTA	CSTTGAGACC	480
CTGGACGACA	TCTTGAGCA	GTGGGCTCAC	TCTGAAGACC	TGCAGTCCCT	CCTGCTTAGG	540
GTCGCTAATG	CTGTTTCGGT	GAAGGGATT	TATAAACAGA	TGCCTGGTT	CTTTAATTTC	600
CTCCGGAAAAA	AACTTTCTT	TTAAACATC	ATAAGGCAG			639

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Leu Ala Leu Leu Glu Leu Ala Arg Gln Asp His Gly Ala Leu						
1	5	10	15			
Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln Ala Ser His						
20	25	30				
Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys Pro Val Ser						
35	40	45				
Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys Pro Ser Leu						
50	55	60				
Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly Gly Glu Gln						
65	70	75	80			
Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu Asp Glu Ser						
85	90	95				
Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln Glu Gly Leu						
100	105	110				
Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro Thr Pro Ser						
115	120	125				
Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val Ser Trp Arg						
130	135	140				
Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp Asp Ile Phe						
145	150	155	160			
Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu Leu Arg Val						
165	170	175				
Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met Pro Gly Cys						
180	185	190				
Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Met						
195	200					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAACGGGGTA CGGCCATGGA CGAAGCGGAT CGGC

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGCTCTAGAT TAGTGGTGGT GGTGGTGGTG TGATTTTA AAGAAAAAGTT TTTCCGGAG

60

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCTCTTTT CCATCCAGGC CGCGGGTGGG GAGCCAGAAGA C

41

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCTTTCTGC TCCCCACCGG CGGCCTGGAT GAAAAAAAGC

39

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCTAGAT TACTTGTCA^T CGTCGTCCTT STAGTCTGAT GTTTAAAGT TAAGTTTTT⁶⁰
CGGGAG⁶⁶

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Arg Gly
1 ^S

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Gly Gly
1 ^S